

### **Amendments to the Claims**

This listing of claims will replace all prior versions and listings of claims in the application.

### **Listing of Claims**

1. (Canceled)
2. (Previously presented) Method according to claim 12, wherein the first and second tissue target cells are malignant cells obtained from solid primary or recurrent tumors, from metastases from such tumors to lymph nodes, blood, bone marrow, blood tissue, liver, lungs, central nervous system, malignant pleural effusions and ascites, urine, cerebral spinal fluid, or other organ sites.
3. (Previously presented) Method according to claim 12, wherein the first and second tissue target cells are malignant cells isolated from single cell suspensions prepared from solid tumor manifestations; and/or from mononuclear cell fractions obtained from bone marrow or blood samples; and/or from cells present in other bodily fluids.
- 4-5. (Canceled)
6. (Previously presented) Method according to claim 12, further comprising the step of cloning RNA and DNA extracted from the isolated cells.
7. (Previously presented) Method according to claim 12, wherein the identification of differential gene expression is determined by differential display or subtractive hybridization.
8. (Previously presented) Method according to claim 7, wherein amplified cDNAs are obtained from malignant cells selected from the first and second tissues and are compared on sequencing gels, and wherein site-specific or site-preferenced patterns revealing differential expression are sequenced and identified.
9. (Previously presented) Method according to claim 8, wherein the expression pattern of identified gene sequences from two or more tumor sites are compared.
- 10-11. (Canceled)

12. (Currently amended) Method for identifying genes differentially expressed between cells isolated from different tissues from the same individual, the method comprising:

(A) detecting target cells from a first and a second tissue, wherein said first and said second tissues are from the same individual;

(B) obtaining nearly 100% specific target cells by repeatedly immunomagnetically isolating, *in vitro*, said first and second tissue target cells;

(C) determining levels of mRNA expression within said first and second tissue target cells;

(D) comparing the levels of mRNA expression in said first and second tissue target cells; and

(E) based upon the comparison in step D, identifying the genes differentially expressed between said first and second tissue target cells, wherein at least one of said first and second tissue target cells are tumor cells, in order to recognize previously unknown genes possibly involved in determining metastatic characteristics of cancer cells.